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The LysE superfamily: topology of the lysine exporter LysE of *Corynebacterium glutamicum*, a paradigm for a novel superfamily of transmembrane solute translocators.

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In *Corynebacterium glutamicum* the LysE carrier protein exhibits the unique function of exporting L-lysine. We here analyze the membrane topology of LysE, a protein of 236 amino acyl residues, using PhoA- and LacZ-fusions. The amino-terminal end of LysE is located in the cytoplasm whereas the carboxy-terminal end is found in the periplasm. Although 6 hydrophobic domains were identified based on hydropathy analyses, only five transmembrane spanning helices appear to be present. The additional hydrophobic segment may dip into the membrane or be surface localized. We show that LysE is a member of a family of proteins found, for example, in *Escherichia coli*, *Bacillus subtilis*, *Mycobacterium tuberculosis* and *Helicobacter pylori*. This family, which we have designated the LysE family, is distantly related to two additional protein families which we have designated the YahN and CadD families. These three families, the members of which exhibit similar sizes, hydropathy profiles, and sequence motifs comprise the LysE superfamily. Functionally characterized members of the LysE superfamily export L-lysine, cadmium and possibly quaternary amines. We suggest that LysE superfamily members will prove to catalyze export of a variety of biologically important solutes.

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